

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.**

Application Serial Number: 10/808,052A  
Source: 1fw0  
Date Processed by STIC: 1/5/05

# ***ENTERED***



IFWO

## RAW SEQUENCE LISTING

DATE: 01/05/2005

PATENT APPLICATION: US/10/808,052A

TIME: 17:00:27

Input Set : A:\18989-033.txt

Output Set: N:\CRF4\01052005\J808052A.raw

3 <110> APPLICANT: Blumberg  
 5 <120> TITLE OF INVENTION: Methods of Inhibiting Inflammation  
 7 <130> FILE REFERENCE: 18989-033  
 9 <140> CURRENT APPLICATION NUMBER: 10/808,052A  
 10 <141> CURRENT FILING DATE: 2004-03-24  
 12 <150> PRIOR APPLICATION NUMBER: 60/457,048  
 13 <151> PRIOR FILING DATE: 2003-03-24  
 15 <160> NUMBER OF SEQ ID NOS: 16  
 17 <170> SOFTWARE: PatentIn Ver. 2.1  
 19 <210> SEQ ID NO: 1  
 20 <211> LENGTH: 21  
 21 <212> TYPE: RNA  
 22 <213> ORGANISM: Artificial Sequence  
 24 <220> FEATURE:  
 25 <223> OTHER INFORMATION: Description of Artificial Sequence:chemically  
 26 synthesized siRNA  
 28 <400> SEQUENCE: 1  
 29 aagcucugga acuaccaacg a 21  
 32 <210> SEQ ID NO: 2  
 33 <211> LENGTH: 21  
 34 <212> TYPE: RNA  
 35 <213> ORGANISM: Artificial Sequence  
 37 <220> FEATURE:  
 38 <223> OTHER INFORMATION: Description of Artificial Sequence:chemically  
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 45 <210> SEQ ID NO: 3  
 46 <211> LENGTH: 3392  
 47 <212> TYPE: DNA  
 48 <213> ORGANISM: Homo sapiens  
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 52 gatgcagttg aggattgctg gtcaatatga ttcttcttgc tgtgcttttt ctctgcttca 120  
 53 tttcctcata ttcagcttct gttaaaggct acacaactgg tctctcatta aataatgacc 180  
 54 ggctgtacaa gctcacgtac tccactgaag ttcttcttga tcggggcaaa ggaaaactgc 240  
 55 aagacagcgt gggctaccgc atttctctca acgtggatgt ggccttacta tggaggaatc 300  
 56 ctgatgggtga tgatgaccag ttgatccaaa taacgatgaa ggatgtaaat gttgaaaatg 360  
 57 tgaatcagca gagaggagag aagagcatct tcaaaggaaa aagcccatct aaaataatgg 420  
 58 gaaaggaaaa cttggaagct ctgcaaagac ctacgctcct tcatctaata catggaaagg 480  
 59 tcaaagagtt ctactcatat caaaatgagg cagtggccat agaaaatata aagagaggtc 540  
 60 tggctagcct atttcagaca cagttaagct ctggaaccac caatgaggta gatattctctg 600  
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62 attcatgcaa aatagcgagg tctggattta cgaccccaaa tcaggctcttg ggtgtcagtt 720
63 caaaagctac atctgtcacc acctataaga tagaagacag ctttggtata gctgtgcttg 780
64 ctgaagaaac acacaatttt ggactgaatt tcctacaaac cattaagggg aaaatagtat 840
65 cgaagcagaa attagagctg aagacaaccg aagcaggccc aagattgatg tctggaaagc 900
66 aggctgcagc cataatcaaa gcagttgatt caaagtacac ggccattccc attgtggggc 960
67 aggtcttcca gagccactgt aaaggatgtc cttctctctc ggagctctgg cgggtccacca 1020
68 ggaaatacct gcagcctgac aacctttcca aggctgaggc tgtcagaaac ttcctggcct 1080
69 tcattcagca cctcaggact gcgaagaaag aagagatcct tcaaatacta aagatggaaa 1140
70 ataaggaagt attacctcag ctggtggatg ctgtcacctc tgctcagacc tcagactcat 1200
71 tagaagccat tttggacttt ttggatttca aaagtgcagc cagcattatc ctccaggaga 1260
72 ggtttctcta tgcctgtgga ttgcttctc atcccaatga agaactcctg agagccctca 1320
73 ttagtaagtt caaaggttct attggtagca gtgacatcag agaaactgtt atgatcatca 1380
74 ctgggacact tgtcagaaag ttgtgtcaga atgaaggctg caaactcaaa gcagtagtgg 1440
75 aagctaagaa gttaatcctg ggaggacttg aaaaagcaga gaaaaagag gacaccagga 1500
76 tgtatctgct ggctttgaag aatgccctgc ttccagaagg catcccaagt cttctgaagt 1560
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83 gatcttcttc tgcctacact ggctacatag aacgtagtcc ccgttcggca tctacttaca 1980
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96 aagagaactc agagatgtgc aaagtgggtg ttgcccctca gccgtagatg acttccagcg 2760
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102 ctagtgtttg ttaaaaacaa aaataaaaac aaaaccacac aaggagaacc caattttgtt 3120
103 tcaacaattt ttgatcaatg tatatgaagc tcttgatagg acttccctta gcatgacggg 3180
104 aaaaccaaac acgttcccta atcaggaaaa aaaaaaaaaa aaaaaagtaa gacacaaaca 3240
105 aaccattttt ttctcttttt ttggagttgg gggcccaggg agaagggaca aggcctttta 3300
106 aagacttggt agccaacttc aagaattaat atttatgtct ctgttattgt tagttttaag 3360
107 ccttaaggta gaaggcat agaaataaca tc 3392
110 <210> SEQ ID NO: 4
111 <211> LENGTH: 894
112 <212> TYPE: PRT

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113 <213> ORGANISM: Homo sapiens
115 <400> SEQUENCE: 4
116 Met Ile Leu Leu Ala Val Leu Phe Leu Cys Phe Ile Ser Ser Tyr Ser
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119 Ala Ser Val Lys Gly His Thr Thr Gly Leu Ser Leu Asn Asn Asp Arg
120           20           25           30
122 Leu Tyr Lys Leu Thr Tyr Ser Thr Glu Val Leu Leu Asp Arg Gly Lys
123           35           40           45
125 Gly Lys Leu Gln Asp Ser Val Gly Tyr Arg Ile Ser Ser Asn Val Asp
126           50           55           60
128 Val Ala Leu Leu Trp Arg Asn Pro Asp Gly Asp Asp Asp Gln Leu Ile
129   65           70           75           80
131 Gln Ile Thr Met Lys Asp Val Asn Val Glu Asn Val Asn Gln Gln Arg
132           85           90           95
134 Gly Glu Lys Ser Ile Phe Lys Gly Lys Ser Pro Ser Lys Ile Met Gly
135           100          105          110
137 Lys Glu Asn Leu Glu Ala Leu Gln Arg Pro Thr Leu Leu His Leu Ile
138           115          120          125
140 His Gly Lys Val Lys Glu Phe Tyr Ser Tyr Gln Asn Glu Ala Val Ala
141           130          135          140
143 Ile Glu Asn Ile Lys Arg Gly Leu Ala Ser Leu Phe Gln Thr Gln Leu
144 145           150          155          160
146 Ser Ser Gly Thr Thr Asn Glu Val Asp Ile Ser Gly Asn Cys Lys Val
147           165          170          175
149 Thr Tyr Gln Ala His Gln Asp Lys Val Ile Lys Ile Lys Ala Leu Asp
150           180          185          190
152 Ser Cys Lys Ile Ala Arg Ser Gly Phe Thr Thr Pro Asn Gln Val Leu
153           195          200          205
155 Gly Val Ser Ser Lys Ala Thr Ser Val Thr Thr Tyr Lys Ile Glu Asp
156           210          215          220
158 Ser Phe Val Ile Ala Val Leu Ala Glu Glu Thr His Asn Phe Gly Leu
159 225           230          235          240
161 Asn Phe Leu Gln Thr Ile Lys Gly Lys Ile Val Ser Lys Gln Lys Leu
162           245          250          255
164 Glu Leu Lys Thr Thr Glu Ala Gly Pro Arg Leu Met Ser Gly Lys Gln
165           260          265          270
167 Ala Ala Ala Ile Ile Lys Ala Val Asp Ser Lys Tyr Thr Ala Ile Pro
168           275          280          285
170 Ile Val Gly Gln Val Phe Gln Ser His Cys Lys Gly Cys Pro Ser Leu
171           290          295          300
173 Ser Glu Leu Trp Arg Ser Thr Arg Lys Tyr Leu Gln Pro Asp Asn Leu
174 305           310          315          320
176 Ser Lys Ala Glu Ala Val Arg Asn Phe Leu Ala Phe Ile Gln His Leu
177           325          330          335
179 Arg Thr Ala Lys Lys Glu Glu Ile Leu Gln Ile Leu Lys Met Glu Asn
180           340          345          350
182 Lys Glu Val Leu Pro Gln Leu Val Asp Ala Val Thr Ser Ala Gln Thr
183           355          360          365
185 Ser Asp Ser Leu Glu Ala Ile Leu Asp Phe Leu Asp Phe Lys Ser Asp

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186	370	375	380
188	Ser Ser Ile Ile Leu Gln Glu Arg Phe Leu Tyr Ala Cys Gly Phe Ala		
189	385	390	395
191	Ser His Pro Asn Glu Glu Leu Leu Arg Ala Leu Ile Ser Lys Phe Lys		
192		405	410
194	Gly Ser Ile Gly Ser Ser Asp Ile Arg Glu Thr Val Met Ile Ile Thr		
195		420	425
197	Gly Thr Leu Val Arg Lys Leu Cys Gln Asn Glu Gly Cys Lys Leu Lys		
198		435	440
200	Ala Val Val Glu Ala Lys Lys Leu Ile Leu Gly Gly Leu Glu Lys Ala		
201		450	455
203	Glu Lys Lys Glu Asp Thr Arg Met Tyr Leu Leu Ala Leu Lys Asn Ala		
204	465	470	475
206	Leu Leu Pro Glu Gly Ile Pro Ser Leu Leu Lys Tyr Ala Glu Ala Gly		
207		485	490
209	Glu Gly Pro Ile Ser His Leu Ala Thr Thr Ala Leu Gln Arg Tyr Asp		
210		500	505
212	Leu Pro Phe Ile Thr Asp Glu Val Lys Lys Thr Leu Asn Arg Ile Tyr		
213		515	520
215	His Gln Asn Arg Lys Val His Glu Lys Thr Val Arg Thr Ala Ala Ala		
216		530	535
218	Ala Ile Ile Leu Asn Asn Asn Pro Ser Tyr Met Asp Val Lys Asn Ile		
219	545	550	555
221	Leu Leu Ser Ile Gly Glu Leu Pro Gln Glu Met Asn Lys Tyr Met Leu		
222		565	570
224	Ala Ile Val Gln Asp Ile Leu Arg Leu Glu Met Pro Ala Ser Lys Ile		
225		580	585
227	Val Arg Arg Val Leu Lys Glu Met Val Ala His Asn Tyr Asp Arg Phe		
228		595	600
230	Ser Arg Ser Gly Ser Ser Ser Ala Tyr Thr Gly Tyr Ile Glu Arg Ser		
231		610	615
233	Pro Arg Ser Ala Ser Thr Tyr Ser Leu Asp Ile Leu Tyr Ser Gly Ser		
234	625	630	635
236	Gly Ile Leu Arg Arg Ser Asn Leu Asn Ile Phe Gln Tyr Ile Gly Lys		
237		645	650
239	Ala Gly Leu His Gly Ser Gln Val Val Ile Glu Ala Gln Gly Leu Glu		
240		660	665
242	Ala Leu Ile Ala Ala Thr Pro Asp Glu Gly Glu Glu Asn Leu Asp Ser		
243		675	680
245	Tyr Ala Gly Met Ser Ala Ile Leu Phe Asp Val Gln Leu Arg Pro Val		
246		690	695
248	Thr Phe Phe Asn Gly Tyr Ser Asp Leu Met Ser Lys Met Leu Ser Ala		
249	705	710	715
251	Ser Gly Asp Pro Ile Ser Val Val Lys Gly Leu Ile Leu Leu Ile Asp		
252		725	730
254	His Ser Gln Glu Leu Gln Leu Gln Ser Gly Leu Lys Ala Asn Ile Glu		
255		740	745
257	Val Gln Gly Gly Leu Ala Ile Asp Ile Ser Gly Ala Met Glu Phe Ser		
258		755	760

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260 Leu Trp Tyr Arg Glu Ser Lys Thr Arg Val Lys Asn Arg Val Thr Val
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263 Val Ile Thr Thr Asp Ile Thr Val Asp Ser Ser Phe Val Lys Ala Gly
264 785      790      795      800
266 Leu Glu Thr Ser Thr Glu Thr Glu Ala Gly Leu Glu Phe Ile Ser Thr
267      805      810      815
269 Val Gln Phe Ser Gln Tyr Pro Phe Leu Val Cys Met Gln Met Asp Lys
270      820      825      830
272 Asp Glu Ala Pro Phe Arg Gln Phe Glu Lys Lys Tyr Glu Arg Leu Ser
273      835      840      845
275 Thr Gly Arg Gly Tyr Val Ser Gln Lys Arg Lys Glu Ser Val Leu Ala
276      850      855      860
278 Gly Cys Glu Phe Pro Leu His Gln Glu Asn Ser Glu Met Cys Lys Val
279 865      870      875      880
281 Val Phe Ala Pro Gln Pro Asp Ser Thr Ser Ser Gly Trp Phe
282      885      890
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286 <211> LENGTH: 2878
287 <212> TYPE: DNA
288 <213> ORGANISM: Mus musculus
290 <400> SEQUENCE: 5
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292 tcctcctact ctgcttccgt taaagggtcac acaactggcc tctcattaaa taatgagcgg 120
293 ctatacaagc tcacgtactc cactgaagtg tttcttgatg ggggcaaaag aaaaccgcaa 180
294 gacagcgtgg gctacaaaat ctcatctgat gtggacgttg tgttactgtg gaggaatcct 240
295 gatggtgatg atgatcaagt gatccaagtc acgataacag ctgttaacgt tgaaaatgcg 300
296 ggtaacacga gaggcgagaa gagcatcttc cagggcaaaa gtacaccta gacataggg 360
297 aaggacaacc tggaggctct gcagagaccc atgcttcttc atctggtccg ggggaaggct 420
298 aaggagtctt actcctatga aaacgagcca gtgggcatag aaaatctcaa gagaggcttg 480
299 gctagcttat tccagatgca gctaagctct ggaactacca acgaggtaga tatctctggg 540
300 gattgtaaag tgacctacca ggcccaacaa gacaaagtgg tcaaaattaa ggctctggat 600
301 acatgcaaaa ttgagcgggtc tggatttaca acggcaaaacc aggtgctggg cgtcagttca 660
302 aaagccacat ctgtcactac ctacaagata gaggacagct ttgtcaccgc tgtgcttgca 720
303 gaagagacca gggcttttgc cttgaacttc caacaaacca tagcaggaaa aatagtgtca 780
304 aagcagaaat tggagctgaa gacaactgaa gccggcccaa ggatgatccc cggaagcaa 840
305 gtggcagggt taattaaagc agttgattcc aaatacaaag ccattcccat tgtgggacag 900
306 gtcctcgagc gtgtctgcaa aggatgccct tctctggcgg agcactggaa gtccatcaga 960
307 aagaacctgg agcctgaaaa cctgtccaag gccgaggctg tccagagctt cctggccttc 1020
308 atccagcacc tccggacttc gaggagagaa gagatcctcc agattctgaa ggcagagaag 1080
309 aaagaagtgc tccctcagct ggtggatgcc gtcacctctg ctgagactcc agactcgcta 1140
310 gaagccatcc tggacttttt ggatttcaaa agtgacagca gtatcatact ccaggaaagg 1200
311 ttcctctatg cctgtggctt tgccaccac cctgatgaag aactcctacg agccctcctt 1260
312 agtaagttca aaggttcctt tgcaagcaac gacatcagag agtcggttat gatcatcatt 1320
313 ggagccctag tcaggaagct gtgtcagaat gaaggctgca agctcaaggc agtgggtgaa 1380
314 gctaagaagc tgatcctggg aggacttgaa aaacagaga agaaagaaga caccacaatg 1440
315 tacctgcttg ccctgaagaa tgccttgctt cccgaaggca tcccgctcct tctgaagtat 1500
316 gctgaggctg gagaagggcc cgtcagccac ctggccacca ctgttctcca gagatacgat 1560
317 gtctccttca tcacagatga ggtgaagaag accttgaaca ggatatacca ccagaatcgt 1620
318 aaggttcatg agaagacggt gcgcacaact gccgctgctg tcatcttaaa gaacccatcc 1680

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Input Set : A:\18989-033.txt  
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:11; Xaa Pos. 14,16,27,31,36,43,47,50,52,53,70,77,81,95,121,123,130,171  
Seq#:11; Xaa Pos. 177,180,197,200,203,204,226,233,241,243,248,261  
Seq#:12; Xaa Pos. 57,67,68,97,99,102,105,106,116,122,149,152,157,163,165  
Seq#:12; Xaa Pos. 173,176,207,214,216,223,229,239,240,251,253,254,257,268  
Seq#:12; Xaa Pos. 270,275,287  
Seq#:13; Xaa Pos. 6,16,17,46,48,51,54,55,63,69,81,84,89,95,97,105,108,133  
Seq#:13; Xaa Pos. 140,142,149,155,162,163,174,176,177,180,191,193,198,202  
Seq#:14; Xaa Pos. 35,41,52,57,58,59,70,72,77,81,82,97,104,108,109,118,126  
Seq#:14; Xaa Pos. 128,131,149,157,166,186,189,195,200,210,219,222,240,252  
Seq#:14; Xaa Pos. 253,261,273,274,297  
Seq#:15; Xaa Pos. 57,67,68,97,99,102,105,106,116,122,149,152,157,163,165  
Seq#:15; Xaa Pos. 173,176,207,214,216,223,229,239,240,251,253,254,257,268  
Seq#:15; Xaa Pos. 270,275,287  
Seq#:16; Xaa Pos. 43,49,60,65,66,67,78,80,85,89,90,105,112,116,117,126,134  
Seq#:16; Xaa Pos. 136,139,157,165,174,194,197,203,208,227,236,239,257,269  
Seq#:16; Xaa Pos. 270,278,290,291,292,314

## VERIFICATION SUMMARY

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Input Set : A:\18989-033.txt

Output Set: N:\CRF4\01052005\J808052A.raw

L:579 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:0  
M:341 Repeated in SeqNo=11  
L:651 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12 after pos.:48  
M:341 Repeated in SeqNo=12  
L:717 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:0  
M:341 Repeated in SeqNo=13  
L:777 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14 after pos.:32  
M:341 Repeated in SeqNo=14  
L:849 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:48  
M:341 Repeated in SeqNo=15  
L:921 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16 after pos.:32  
M:341 Repeated in SeqNo=16